

RAW SEQUENCE LISTING

EFS

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/574,639
Source: IFW0
Date Processed by STIC: 3/2/07

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 03/02/2007

PATENT APPLICATION: US/10/574,639

TIME: 12:58:04

Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt

Output Set: N:\CRF4\03022007\J574639.raw

3 <110> APPLICANT: Thiry, Michel
 4 Dheur, Ingrid
 6 <120> TITLE OF INVENTION: Piscirickettsia Salmonis Antigens and Use Thereof
 8 <130> FILE REFERENCE: 425.1018
 10 <140> CURRENT APPLICATION NUMBER: 10/574,639
 C--> 11 <141> CURRENT FILING DATE: 2006-03-31
 13 <150> PRIOR APPLICATION NUMBER: PCT/IB2004/03339
 14 <151> PRIOR FILING DATE: 2004-10-01
 16 <150> PRIOR APPLICATION NUMBER: 2003/0743
 17 <151> PRIOR FILING DATE: 2003-10-07
 19 <160> NUMBER OF SEQ ID NOS: 19
 21 <170> SOFTWARE: PatentIn version 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1314
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Piscirickettsia salmonis
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1314)
 33 <400> SEQUENCE: 1
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 36 1 5 10 15
 38 gcg act gcc gca aat gcc gct gat aat ggt aag ctt caa tta caa atc 96
 39 Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
 40 20 25 30
 42 aac caa ttg aag gcg caa cac act caa ctt caa cag caa gtt gct aat 144
 43 Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Gln Val Ala Asn
 44 35 40 45
 46 ctg caa ggt caa ggc caa act act ggt gcc gtt cac gtt ggc gct gtt 192
 47 Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
 48 50 55 60
 50 ggt ggt gaa cta atc tct gaa aat aac tac gat ggt cgt ggc tta gat 240
 51 Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
 52 65 70 75 80
 54 ctt ctt aaa tca tta gcg aaa gca ggc agc aat gca ccg tta tta act 288
 55 Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
 56 85 90 95
 58 att ggt ggt acg tta gaa gct gat gcg caa atg aac cgt aac ggt aat 336
 59 Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
 60 100 105 110
 62 gtt gga tct ggt tct act tct ggt gac cct tct ggc ctt aac tat act 384
 63 Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr

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66	gat gga act agc agt tct gca ttc tat tta gat act gca cgt att gat	432		
67	Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp			
68	130	135	140	
70	atc tta gcg cat gtg aat gac tgg gtt aac ggt gaa atc tcg tat gac	480		
71	Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp			
72	145	150	155	160
74	tta aat ggt gat agt ggt ctt cac act ggt agc ctt tta gtg ggt aac	528		
75	Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn			
76	165	170	175	
78	ctc aat caa tta cca gtt tat ggt caa atc ggt aaa ttc tac cca gat	576		
79	Leu Asn Gln Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp			
80	180	185	190	
82	gca ggt ttg ttt gaa tta gct agt gat gat gtt tat tct tct agc tta	624		
83	Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu			
84	195	200	205	
86	gtc aag cgt tat ttc cgt cca gat gcg caa aat ggt gca tct gta ggc	672		
87	Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly			
88	210	215	220	
90	ttc tat aaa gca ggc tta cat act tct tta act gca ttt aaa acg tct	720		
91	Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser			
92	225	230	235	240
94	gct cca caa gct aat gct gct aac tat aac caa gca act agt gat tgg	768		
95	Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp			
96	245	250	255	
98	tct gca caa gcg gat tac act ttt aat gca ggt caa gtc aat gcc act	816		
99	Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr			
100	260	265	270	
102	ata ggt gca ggt tac tta tct aat atg gtg aat acc aat gac agc ttc	864		
103	Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe			
104	275	280	285	
106	act gca aca ggt gca gga act ggt aca caa aaa gat cgg cta ccg atg	912		
107	Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met			
108	290	295	300	
110	gct aat gta agc gct aag att ggc ttt ggt cca ttt gaa gcc ctt gct	960		
111	Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala			
112	305	310	315	320
114	act tat gct caa aca tta aaa ggt ttg gcg aat act aca ggt ggt aca	1008		
115	Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr			
116	325	330	335	
118	acg aag ttg aaa gcc ttt gat tta gaa ggt gct tac cac ttc caa gct	1056		
119	Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala			
120	340	345	350	
122	gtg aag ccg atg act gtg atg tta ggt tat agc cgt aca tat ggc ttt	1104		
123	Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe			
124	355	360	365	
126	gat aag gtt gga cct gtt gat cag ttt att gat ggt aat act gcg att	1152		
127	Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile			
128	370	375	380	

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130 act atc aat aac aaa aaa gac caa tgg tta ttg ggt gta aac tct gaa      1200
131 Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Leu Gly Val Asn Ser Glu
132 385                               390                               395                               400
134 gta ttt aag aac aca acg gtt ggt ctt gag tat gcg cgt gta ggt cag      1248
135 Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln
136                               405                               410                               415
138 ctt gat agc aca ggt act gac act aac cgc tac aac gta ttg act gcg      1296
139 Leu Asp Ser Thr Gly Thr Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala
140                               420                               425                               430
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143 Asp Met Thr Val Lys Phe
144                               435
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148 <211> LENGTH: 438
149 <212> TYPE: PRT
150 <213> ORGANISM: Piscirickettsia salmonis
152 <400> SEQUENCE: 2
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158 Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
159                               20                               25                               30
162 Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Gln Val Ala Asn
163                               35                               40                               45
166 Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
167                               50                               55                               60
170 Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
171 65                               70                               75                               80
174 Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
175                               85                               90                               95
178 Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
179                               100                              105                              110
182 Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr
183                               115                              120                              125
186 Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp
187                               130                              135                              140
190 Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp
191 145                              150                              155                              160
194 Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn
195                               165                               170                               175
198 Leu Asn Gln Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp
199                               180                              185                              190
202 Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu
203                               195                              200                              205
206 Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly
207                               210                              215                              220
210 Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser
211 225                              230                              235                              240
214 Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp
215                               245                              250                              255

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218 Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr
219                260                265                270
222 Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe
223                275                280                285
226 Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met
227                290                295                300
230 Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala
231 305                310                315                320
234 Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr
235                325                330                335
238 Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala
239                340                345                350
242 Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe
243                355                360                365
246 Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile
247                370                375                380
250 Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Leu Gly Val Asn Ser Glu
251 385                390                395                400
254 Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln
255                405                410                415
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267 <211> LENGTH: 1248
268 <212> TYPE: DNA
269 <213> ORGANISM: Piscirickettsia salmonis
272 <220> FEATURE:
273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)..(1248)
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279 1                5                10                15
281 cac act caa ctt caa cag caa gtt gct aat ctg caa ggt caa ggc caa      96
282 His Thr Gln Leu Gln Gln Gln Val Ala Asn Leu Gln Gly Gln Gly Gln
283                20                25                30
285 act act ggt gcc gtt cac gtt ggc gct gtt ggt ggt gaa cta atc tct      144
286 Thr Thr Gly Ala Val His Val Gly Ala Val Gly Gly Glu Leu Ile Ser
287                35                40                45
289 gaa aat aac tac gat ggt cgt ggc tta gat ctt ctt aaa tca tta gcg      192
290 Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp Leu Leu Lys Ser Leu Ala
291                50                55                60
293 aaa gca ggc agc aat gca ccg tta tta act att ggt ggt acg tta gaa      240
294 Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr Ile Gly Gly Thr Leu Glu
295 65                70                75                80
297 gct gat gcg caa atg aac cgt aac ggt aat gtt gga tct ggt tct act      288
298 Ala Asp Ala Gln Met Asn Arg Asn Gly Asn Val Gly Ser Gly Ser Thr

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302	Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr Asp Gly Thr Ser Ser Ser							
303		100		105		110		
305	gca ttc tat tta gat act gca cgt att gat atc tta gcg cat gtg aat							384
306	Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp Ile Leu Ala His Val Asn							
307		115		120		125		
309	gac tgg gtt aac ggt gaa atc tcg tat gac tta aat ggt gat agt ggt							432
310	Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp Leu Asn Gly Asp Ser Gly							
311		130		135		140		
313	ctt cac act ggt agc ctt tta gtg ggt aac ctc aat caa tta cca gtt							480
314	Leu His Thr Gly Ser Leu Leu Val Gly Asn Leu Asn Gln Leu Pro Val							
315	145		150		155		160	
317	tat ggt caa atc ggt aaa ttc tac cca gat gca ggt ttg ttt gaa tta							528
318	Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp Ala Gly Leu Phe Glu Leu							
319		165		170		175		
321	gct agt gat gat gtt tat tct tct agc tta gtc aag cgt tat ttc cgt							576
322	Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu Val Lys Arg Tyr Phe Arg							
323		180		185		190		
325	cca gat gcg caa aat ggt gca tct gta ggc ttc tat aaa gca ggc tta							624
326	Pro Asp Ala Gln Asn Gly Ala Ser Val Gly Phe Tyr Lys Ala Gly Leu							
327		195		200		205		
329	cat act tct tta act gca ttt aaa acg tct gct cca caa gct aat gct							672
330	His Thr Ser Leu Thr Ala Phe Lys Thr Ser Ala Pro Gln Ala Asn Ala							
331		210		215		220		
333	gct aac tat aac caa gca act agt gat tgg tct gca caa gcg gat tac							720
334	Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp Ser Ala Gln Ala Asp Tyr							
335	225		230		235		240	
337	act ttt aat gca ggt caa gtc aat gcc act ata ggt gca ggt tac tta							768
338	Thr Phe Asn Ala Gly Gln Val Asn Ala Thr Ile Gly Ala Gly Tyr Leu							
339		245		250		255		
341	tct aat atg gtg aat acc aat gac agc ttc act gca aca ggt gca gga							816
342	Ser Asn Met Val Asn Thr Asn Asp Ser Phe Thr Ala Thr Gly Ala Gly							
343		260		265		270		
345	act ggt aca caa aaa gat cgg cta ccg atg gct aat gta agc gct aag							864
346	Thr Gly Thr Gln Lys Asp Arg Leu Pro Met Ala Asn Val Ser Ala Lys							
347		275		280		285		
349	att ggc ttt ggt cca ttt gaa gcc ctt gct act tat gct caa aca tta							912
350	Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala Thr Tyr Ala Gln Thr Leu							
351		290		295		300		
353	aaa ggt ttg gcg aat act aca ggt ggt aca acg aag ttg aaa gcc ttt							960
354	Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr Thr Lys Leu Lys Ala Phe							
355	305		310		315		320	
357	gat tta gaa ggt gct tac cac ttc caa gct gtg aag ccg atg act gtg							1008
358	Asp Leu Glu Gly Ala Tyr His Phe Gln Ala Val Lys Pro Met Thr Val							
359		325		330		335		
361	atg tta ggt tat agc cgt aca tat ggc ttt gat aag gtt gga cct gtt							1056
362	Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe Asp Lys Val Gly Pro Val							
363		340		345		350		

VERIFICATION SUMMARY

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Input Set : N:\efs\03_02_07\10574639_efs\seqlisting.txt

Output Set: N:\CRF4\03022007\J574639.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:496 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:501 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:506 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:511 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:516 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
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L:542 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (14) SEQUENCE:
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